

HeatMap

 Michael Henderson

Updated date: Jun 22, 2022

 An abbreviated version of this protocol was published in Science Advances in Jun 2021

Computational modeling of tau pathology spread reveals patterns of regional vulnerability and the impact of a genetic risk factor

DOI: [10.1126/sciadv.abg6677](https://doi.org/10.1126/sciadv.abg6677)

Related files

 HeatMap.pdf



How to cite: (Readers should cite both the Bio-protocol preprint and the original research article where this protocol was used)

1. Henderson, M. (2022). HeatMap. Bio-protocol Preprint. bio-protocol.org/prep1737.
2. Cornblath, E. J., Li, H. L., Changoikar, L., Zhang, B., Brown, H. J., Gathagan, R. J., Olufemi, M. F., Trojanowski, J. Q., Bassett, D. S., Lee, V. M. Y. and Henderson, M. X. (2021). Computational modeling of tau pathology spread reveals patterns of regional vulnerability and the impact of a genetic risk factor. Science Advances 7(24). DOI: [10.1126/sciadv.abg6677](https://doi.org/10.1126/sciadv.abg6677)

Copyright: Content may be subjected to copyright.